

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	101.6	4.9	991	4	US-09-377-648-7	Sequence 7, Appli
2	62.4	3.0	718	1	US-08-232-463-14	Sequence 14, Appl
3	41	2.0	1318	2	US-08-439-814-3	Sequence 3, Appli
4	41	2.0	1888	2	US-08-439-814-2	Sequence 2, Appli
5	41	2.0	2090	2	US-08-439-814-1	Sequence 1, Appli
6	39	1.9	19124	2	US-08-487-8268-13	Sequence 13, Appl
7	38.4	1.9	1931	4	US-09-118-442-10	Sequence 10, Appl
8	38.4	1.9	1931	4	US-09-677-064-10	Sequence 10, Appl
9	37.8	1.8	5822	4	US-09-067-800-3	Sequence 3, Appli
10	37.8	1.8	5622	4	US-09-349-677-3	Sequence 3, Appli
11	37.4	1.8	5852	1	US-07-867-106-2	Sequence 2, Appli
12	37.2	1.8	602	1	US-07-764-100-8	Sequence 8, Appli
13	37.2	1.8	643	1	US-08-764-100-7	Sequence 7, Appli
14	37.2	1.8	688	4	US-08-998-416-972	Sequence 972, Appl
15	37.2	1.8	740	4	US-08-998-416-971	Sequence 971, Appl
16	37.2	1.8	2993	1	US-08-764-100-2	Sequence 2, Appli
17	37.2	1.8	2993	1	US-08-764-100-10	Sequence 10, Appl
18	37.2	1.8	3001	1	US-08-764-100-1	Sequence 1, Appli
19	36.8	1.8	701	4	US-08-998-416-701	Sequence 701, Appl
20	36	1.7	2621	2	US-08-553-6198-8	Sequence 8, Appli
21	36	1.7	7015	4	US-09-177-249-6	Sequence 6, Appli
22	35.8	1.7	2730	2	US-08-811-897A-39	Sequence 39, Appli
23	35.8	1.7	2730	2	US-08-855-213-39	Sequence 39, Appl
24	35.8	1.7	2814	2	US-08-811-897A-38	Sequence 38, Appl
25	35.8	1.7	2814	2	US-08-855-213-38	Sequence 38, Appl
26	35.8	1.7	6769	1	US-08-480-784-20	Sequence 20, Appl
27	35.8	1.7	6769	1	US-08-483-553-20	Sequence 20, Appl

	Query Match	2.0%;	Score 41;	DB 2;	Length 16880;
	Best Local Similarity	63.9%;	Pred. N.0.046;		
	Matches 62;	Conservative 0;	Mismatches 35;	Indels	
QY	702	atgttaaacattt	tagtaataatt	tgttagcattt	taagtctctacgaatttatg
Db	832	ATATTAAATGT	TGGCAGTAAAT	TATGGAAGAAAT	TACAACTAATGTAATGCTGCT
QY	762	tgtagtattgtt	tatatcaattt	taataaaactgtaa	798
Db	892	TGCTATGTTT	TATTACTAAAT	TTTGTAATAAAATGTA	928

RESULT 5
US-08-439-814-1
; Sequence 1, Application US/08439814
; Patent No. 5968735
; GENERAL INFORMATION:
; APPLICANT: STEIN, Ulrike
; APPLICANT: WALTHERR, Wolfgang
; TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF
; TITLE OF INVENTION: THERAPY-RELEVANT GENES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAI DO, MARWELSTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth Street, N. W., Suite 330 G
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/439,814
; FILING DATE: 12-MAY-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 4238778.7
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE PCT/DE93/01086
; FILING DATE: 10-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KLESNER, Sharon N.
; REGISTRATION NUMBER: 36,335
; REFERENCE/DOCKET NUMBER: P1614-5015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P4238778.7
; FILING DATE: 12-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/DE93/01086
; FILING DATE: 10-NOV-1993
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2090 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

```
; MOLECULE TYPE: DNA (genomic)
US-08-439-814-1

Query Match          2.0%; Score 41; DB 2; Length 2090;
Best Local Similarity 63.9%; Pred No. 0.053;
Matches 62; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

Qy   702 atgttaaacatttgtagtaaataatgctgcagcattttacgtctcacgaatttatggaaaaa 761
      ||||| | | ||||||| | | |||| | | | | |||| | | | | |||| |
Db   1234 ATATTAAGTTGGCAGTAAATAATGAAGAAGAAATTACAACCTAATGTAATGTCTAAAACA 1293
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy   762 tgtagtgtgttcatataaatTTTTTaataaaactgtaa 798
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   1294 TCGTAGTTTATTTACTAATTTCAATTTAAAAATGTAA 1330
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT        6
US-08-487-826B-13
; Sequence 13, Application US/08487826B
; Patent No. 5993827
; GENERAL INFORMATION:
; APPLICANT: Sim, Kim L.
; APPLICANT: Chitnis, Chetan
; APPLICANT: Miller, Louis H.
; APPLICANT: Peterson, David S.
; APPLICANT: Su, Xin-zhaun
; APPLICANT: Wellemis, Thomas E.
; TITLE OF INVENTION: BINDING DOMAINS FROM PLASMODIUM VIVAX
; AND PLASMODIUM FALCIPIPARUM ERYTHROCYTE BINDING PROTEINS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe Martens Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: California
; COUNTRY: US
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,826B
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Israelisen, Ned
; REGISTRATION NUMBER: 29,655
; REFERENCE/DOCKET NUMBER: NIH121.001CP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 235-8550
; TELEFAX: (619) 235-0176
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19124 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; HYPOTHEetical: NO
; ANTI-SENSE: NO
US-08-487-826B-13

Query Match          1.9%; Score 39; DB 2; Length 19124;
Best Local Similarity 46.5%; Pred No. 1;
Matches 126; Conservative 0; Mismatches 145; Indels 0; Gaps 0;

Qy   529 taagaacagatgatgtatgacctgaccgtgacgttcacaaggcccaaaaaaaaaacttgt 588
      ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   15604 TAAGAAAAAAAAATTTTATATAAAAAAAAAAATGATTATATAAAAAATAAAAAACAAAGAAGAA 15663
```


[illegible]

RESULTS 11
US-07867-106-2/c
; Sequence 2, Application US/07867106
; Patent No. 5389526
; GENERAL INFORMATION:
; APPLICANT: Slade, Martin B
; APPLICANT: Chang, Andy C M
; APPLICANT: Williams, Keith L
; TITLE OF INVENTION: Improved Plasmid Vectors for Cellular
; TITLE OF INVENTION: Slime Moulds of the Genus Dictyostelium
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSSE: Woodcock Washburn Kurtz Mackiewicz & No. 5389526r1s
; STREET: One Liberty Place 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103

Query Match 1.88; Score 37.4; DB 1; Length 5852;
Best Local Similarity 46.6%; Pred. NO. 1.3;
Matches 156; Conservative 0; Mismatches 176; Indels 3; Gaps 1;

Qy	6	atttttttccaa	ctcccccggag	ttaatatccaa	tctaaaaatcaggagaaatt	65						
Db	1952	AGTTTTTTAT	AGTTTTTGGCAT	TTTTAAAAAAT	AACTTTTAAATTTTAAATTTGATTTTTTAAT	18993						
Qy	66	atatggccata	tattatagaagc	aactaaataa	aaatgtgggtt	gtgtattgaa	aaaaaaaccta	125				
Db	1892	ATGAGATCT	AAATAAAAA	AAAAAATTTT	AAAAATTTTAAAAA	AAAAAAGAAAAA	AAAAA	1833				
Qy	126	ttatacaaa	catctgcga	gaatacaat	tc--ttttat	cacaaacttat	atgtgagt	182				
Db	1832	AGTAGAA	TTTTTAAAAA	TTAAATAT	TATTAATTC	TTAAATTAAT	TATATTCGAT	1773				
Qy	183	tcttttctct	gtgaactct	tataataa	aacattttt	ggctataa	aatggc	aaacta	242			
Db	1772	AGCAAT	TTATTTTAT	CTATCTAT	AAAAA	AAACTAG	AAAAATGA	ATGTCATCA	ATTA	1713		
Qy	243	agttagc	accactg	taattaga	attt	gtctgg	aaacaattt	ctctgact	taagaagct	tattt	302	
Db	1712	GTA	TTTTTA	CAATTTTT	TTTTTTTT	TTTTTTTT	AAAAA	AAAGTGC	ATGAC	AAAAA	AAAG	1653
Qy	303	ggactgt	ctcttttgc	caacaag	tag	gaaaatg	gaa					337
Db	1652	TGTCATG	CAAAAAA	AAAAA	AAAAA	AAAAA	AAAGAGG	GGAA				1618

RESULT 12
US-08-764-100-8/c
; Sequence 8, Application US/08764100
; Patent No. 5773700
; GENERAL INFORMATION:
; APPLICANT: van Grinsven J., Martinus Q.
; APPLICANT: De Haan, Petrus T.
; APPLICANT: Gielen L., Johannes J.
; APPLICANT: Peters, Dirk
; APPLICANT: Goldbach, Robert W.
; TITLE OF INVENTION: Improvements in or Relating to Organic
; TITLE OF INVENTION: Compounds
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sandoz Agro, Inc
; STREET: 975 California Avenue
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/764,100
; FILING DATE: 06-DEC-1996
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/214,064
; FILING DATE:
; APPLICATION NUMBER: US 08/032,235
; FILING DATE: 17-MAR-1993
; APPLICATION NUMBER: GB 9206016.9
; FILING DATE: 19-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: NO. 5773700r/s, Allen E.
; REGISTRATION NUMBER: 34,490
; REFERENCE/DOCKET NUMBER: 137-1061
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 354-3592
; TELEFAX: (415) 857-1125
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 602 base pairs
; TYPE: nucleic acid

```

; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-764-100-8

```

Query Match 1.8%; Score 37.2; DB 1; Length 602;
Best Local Similarity 49.0%; Pred. No. 0.3;
Matches 99; Conservative 0; Mismatches 103; Indels

[illegible]

```

RESULT 13
US-08-764-100-7/c
; Sequence 7, Application US/08764100
; Patent No. 5773700
; GENERAL INFORMATION:
; APPLICANT: van Grinsven J., Martinus Q.
; APPLICANT: De Haan, Petrus T.
; APPLICANT: Gielen L., Johannes J.
; APPLICANT: Peters, Dirk
; APPLICANT: Goldbach, Robert W.
; TITLE OF INVENTION: Improvements in or Relating to Organic Compounds
; TITLE OF INVENTION: Compounds

```

ADDRESSEE: Sandoz Agro, Inc
STREET: 975 California Avenue
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

```

:
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/764,100
: FILING DATE: 06-DEC-1996
: CLASSIFICATION: B00
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/214,064
:

```

FILING DATE: 05/06/1993
 APPLICATION NUMBER: US 08/032,235
 FILING DATE: 17-MAR-1993
 APPLICATION NUMBER: GB 9206016.9
 FILING DATE: 19-MAR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: No. 577370Dris, Allen E.
 REGISTRATION NUMBER: 34,490
 REFERENCE/DOCKET NUMBER: 137-1061
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 354-3592
 TELEFAX: (415) 857-1125
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 643 base/pairs
 TYPE: nucleic acid

```

; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-764-100-7

```

Query Match	1.8%	Score 37.2;	DB 1;	Length 643;
Best Local Similarity	49.0%;	Pred. No. 0.31;		
Matches 99;	Conservative	0;	Mismatches 103;	Indels 0;
				Gaps 0;

Qy	113	aaaaaaacactattataacaacatctgcgaagaatacaattcttttatacacaactt	172
Db	315	AAAAAACAACAAAACAAAACAAAACAAAACAAATTTTTGGCCAAATT	256
Qy	173	atatgtgagtgcttttctctctgtaactcttatataaaaacatttttggctattaaata	232
Db	255	GTGAGTAGATTGGATTTAAAGTTTATAATTACTAATACATTCATTTTAAAGCATTTATTA	196
Qy	233	atgscactaatgttagcacacagtgaattagatttgtctggacaacattctctgactaa	292
Db	195	AAGCAACCAAATGTGCCGAAGCCATCCTTTTTTGTTTTTATTTATTTATGATTTT	136
Qy	293	gaagctatttggactgtccctt	314
Db	135	TTTTTGTATTTTATATATATATTTT	114

```

RESULT 14
US-08-998-416-972/C
; Sequence 972, Application US/08998416
; Patent No. 6239264
;
; GENERAL INFORMATION:
; APPLICANT: Philippssen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jorgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Rebischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
;

```

ADDRESSEE: NO. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NO. 6239264th Carolina
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFAX: 919-541-8689
INFORMATION FOR SEO ID NO: 972:

```

; INFORMATION FOR SEQ ID NO: 972:
;
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 688 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear

```

; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE: PAG1598UP
; ORGANISM: PAG1598RP
US-08-998-416-972

Query Match 1.8%; Score 37.2; DB 4; Length 688;
Best Local Similarity 48.2%; Pred. No. 0.33;
Matches 105; Conservative 0; Mismatches 113; Indels 0; Gaps 0;
QY 42 acaatcctaaatcaggagaaatttatatgcccattatagagcaactaaataaaatgt 101
Db 443 ATACATACTATTACTAAATTAATAATAATTTGATTTCTATATGCCATATATTTT 384
QY 102 gcgttgattgaaaaaaacccattttaacaaacatctgccagaataacaaattctttt 161
Db 383 ATTATTAAATATTATTAAATTTATTATTAAATAATTAGATTATAATTAATCTTTTA 324
QY 162 atacaaacttatatgaggtcttttctctgttaactcttataataaaacatttttg 221
Db 323 TAATAAATTTATATTATTAAATTAATATATTAATTTATTATTATTATTATTATTA 264
QY 222 gctattcaataatggcaactaagttgacaccactgtaa 259
Db 263 TATAATCTTTATAGGAATTAACCTTAATAAACCAATTAA 226

RESULT 15

US-08-998-416-971
; Sequence 971, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippsen, Peter
; APPLICANT: Pohlmann, Rainer
; APPLICANT: Steinert, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jurgen
; APPLICANT: Knechtie, Philipp
; APPLICANT: Reibschung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPHII
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6239264artis Corporation
; STREET: 3054 Cornwalis Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998.416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 971:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 740 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single

; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE: PAG1598RP
; ORGANISM: PAG1598RP
US-08-998-416-971

Query Match 1.8%; Score 37.2; DB 4; Length 740;
Best Local Similarity 49.0%; Pred. No. 0.35;
Matches 99; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY 42 acaatcctaaatcaggagaaatttatatgcccattatagagcaactaaataaaatgt 101
Db 451 ATACATACTATTACTAAATTAATAATAATTTGATTTCTATATGCCATATATTTT 510
QY 102 gcgttgattgaaaaaaacccattttaacaaacatctgccagaataacaaattctttt 161
Db 511 ATTATTAAATTTATTATTAAATTTATTATTAAATAATTAATTAATTAATCTTTTA 570
QY 162 atacaaacttatatgaggtcttttctctgttaactcttataataaaacatttttg 221
Db 571 TAATAAATTTATATTATTAAATTAATTAATTAATTTATTATTATTATTATTATTA 630
QY 222 gctattcaataatggcaactaa 243
Db 631 TATAATCTTTTATAGGAATTTGA 652

Search completed: December 19, 2001, 22:39:44
Job time: 5729 sec

[illegible]

[illegible]

QY 872 tgcgtctgcgaa 884
LOCUS : : l
Db 1112 NNNNNNTMRA 1124

RESULT 8
AL354718
DEFINITION Human DNA sequence from clone RP11-187C18 on chromosome 9, complete sequence.
ACCESSION AL354718 AC027516
VERSION AL354718.10 GI:13751347
KEYWORDS HTG.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 175271)
Direct Submission
Submitted (31-MAY-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
On May 15, 2001 this sequence version replaced gi:7677898
gi:13443354.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest. The following
abbreviations are used to associate primary accession numbers given
in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP
database can be found at
<http://www.sanger.ac.uk/projects/Celegans/wormpep> This sequence
was generated from part of bacterial clone contigs of human
chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping
Group. Further information can be found at
<http://www.sanger.ac.uk/HGP/Chr9>
RP11-187C18 is from the library RPCI-11.1 constructed by the group
of Pieter de Jong. For further details see
<http://www.chori.org/bacpac/home.htm>
VECTOR: pBAC3.6
This sequence is the entire insert of clone RP11-187C18.

FEATURES
Location/Qualifiers
1..175271
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="9"
/clone="RP11-187C18"
/clone.lib="RPCI-11.1"
443..874
/note="LTR16B repeat: matches 17. .455 of consensus"
repeat_region
2184..2357
/note="MER45 repeat: matches 4. .178 of consensus"
repeat_region
4701..4918
/note="L2 repeat: matches 301. .514 of consensus"
repeat_region
5526..5759
/note="MLTID repeat: matches 227. .477 of consensus"
repeat_region
5760..5972
/note="L1NA6 repeat: matches 6086. .6299 of consensus"
repeat_region
5973..6220
/note="MLTID repeat: matches 33. .227 of consensus"
repeat_region
6221..6573

/note="THE1B repeat: matches 1. .364 of consensus"
6574..6604
/note="MLTID repeat: matches 1. .33 of consensus"
6816..6869
/note="27 copies 2 mer tt 75% conserved"
7939..8032
/note="MIR repeat: matches 103. .197 of consensus"
8040..8355
/note="AluSk repeat: matches 1. .305 of consensus"
9192..9826
/note="L1PA8 repeat: matches 5522. .6163 of consensus"
10472..10885
/note="L1ME1 repeat: matches 4755. .5173 of consensus"
10894..12930
/note="L1PA7 repeat: matches 4089. .6144 of consensus"
13015..13607
/note="MER77 repeat: matches 28. .632 of consensus"
13635..14266
/note="L1ME1 repeat: matches 5263. .5937 of consensus"
15917..16183
/note="L1M4 repeat: matches 5531. .5801 of consensus"
20329..20410
/note="41 copies 2 mer at 65% conserved"
21467..21881
/note="MER74A repeat: matches 119. .558 of consensus"
22262..22359
/note="L1ME repeat: matches 5544. .5641 of consensus"
22462..22760
/note="AluSk repeat: matches 1. .299 of consensus"
23639..23820
/note="MLTIA2 repeat: matches 6. .180 of consensus"
23829..23866
/note="19 copies 2 mer ct 78% conserved"
23901..24046
/note="MLTIA2 repeat: matches 238. .388 of consensus"
24845..25780
/note="L1PA16 repeat: matches 2983. .3906 of consensus"
25781..26078
/note="AluY repeat: matches 1. .310 of consensus"
26079..28287
/note="L1PA16 repeat: matches 3906. .6157 of consensus"
28347..28864
/note="MER74A repeat: matches 1. .532 of consensus"
29272..29701
/note="MER89 repeat: matches 28. .559 of consensus"
29702..29957
/note="L1M4 repeat: matches 4006. .4273 of consensus"
29960..30009
/note="25 copies 2 mer ta 100% conserved"
30047..30260
/note="MER46A repeat: matches 1. .214 of consensus"
30380..30518
/note="MER67A repeat: matches 404. .543 of consensus"
30519..30798
/note="L1PA16 repeat: matches 5869. .6150 of consensus"
30825..31252
/note="L1M4 repeat: matches 4323. .4755 of consensus"
31417..31520
/note="AluJo/FRAM repeat: matches 159. .267 of consensus"
31955..32776
/note="L1ME2 repeat: matches 5345. .6136 of consensus"
36345..36566
/note="L1ME repeat: matches 5562. .5789 of consensus"
37479..37800
/note="MER58B repeat: matches 1. .336 of consensus"
37867..37917
/note="MER58 repeat: matches 2244. .2294 of consensus"
37967..38261
/note="AluSp repeat: matches 1. .297 of consensus"
38851..39159
/note="AluSp repeat: matches 1. .313 of consensus"
41712..42193
/note="L1MA5 repeat: matches 5823. .6300 of consensus"


```
misc_feature 1..33392
/note="assembly_fragment:01246
fragment_chain:1
clone_end:T7
vector_side:left"
33493..40657
/note="assembly_fragment:00130
fragment_chain:1"
40758..128769
/note="assembly_fragment:01367
fragment_chain:1
clone_end:SP6
vector_side:right"
BASE COUNT 40059 a 24900 c 24955 g 38655 t 200 others
ORIGIN

Query Match 2.9%; Score 59.2; DB 2; Length 128769;
Best Local Similarity 38.3%; Pred. No. 0.0074;
Matches 297; Conservative 0; Mismatches 478; Indels 1; Gaps 1;

Qy 1 tctagattttttcaattcaccgccgagtaaatcccaatcctcaaaatcaggag 60
Db 40997 TATAAATTTATAAATAATATAAATAATATAAATAATATAAATAATATAA 40938

Qy 61 aaattataggccattattatagaagcaactaaataaaatgtgcgttattgaaaaaaa 120
Db 40937 ATATATTATATATATATATATATATATATATATATATATATATATATATAT 40878

Qy 121 acctattatacaaaacatcgcgaagatacaaatctttttatcacacaacttatatgta 180
Db 40877 ATATAAATATATATATATATATATATATATATATATATATATATATATATATA 40818

Qy 181 gtctttctcttgaactcttataaataaacatttttggctattaaataaaggcaac 240
Db 40817 TATATATTATATATATATATATATATATATATATATATATATATATATATAA 40758

Qy 241 taagttagcaccactgtaatlagattttgtctggacaattctctgactaagaagctat 300
Db 40757 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 40698

Qy 301 ttggactgtcctttgccaacaagtagaaaatggaaacgcgtccttcaaaacattctc 360
Db 40697 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 40638

Qy 361 acatgcgtgggtgcgtgaataaaactgaacattagctttttatagctctgcgtctcgc 420
Db 40637 ATATATATATATATATATATATATATATATATATATATATATATATATATAT 40579

Qy 421 tagtatgtttataaaatcattttaccattaccccttttttaataactgtacgtatttca 480
Db 40578 AAATATATATATATATATATATATATATATATATATATATATATATATATATA 40519

Qy 481 tcagtagaactactcacggagcgtcaaaacaaacaaagttgttctactgataaaagcagaga 540
Db 40518 TATATAAATATATATATATATATATATATATATATATATATATATATATATATAT 40459

Qy 541 tgatgtagccgtgacccgtgagctaaaagtccaaaaaaaactgctcccaataacga 600
Db 40458 AAATATAAATATATATATATATATATATATATATATATATATATATATATAT 40399

Qy 601 caaaacaagtgttattgtatggcctaaattacagcacactgacaccacacgtattatt 660
Db 40398 ATAAAAATATATATATATATATATATATATATATATATATATATATATATATA 40339

Qy 661 tctctccattatacaacaggatgtaactgtaaaaattttgtatgtttaaacatttgtagta 720
Db 40338 TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 40279

Qy 721 aatattgtcagcatttcacgtctaacgaatttattgaaaaaaatgtagtagttgtttta 776
Db 40278 TTCCTCCTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTTTATGTT 40223
```

```
RESULT 10
AB035880/c
LOCUS
DEFINITION Chaitoregma tattakana mitochondrial genes for small subunit rRNA,
trRNA-Val, large subunit rRNA, partial and complete sequences.
ACCESSION AB035880
VERSION AB035880.1 GI:13488781
KEYWORDS trRNA-Val; large subunit rRNA; small subunit rRNA; small subunit
ribosomal RNA; large subunit ribosomal RNA.
SOURCE Chaitoregma tattakana mitochondrion DNA.
ORGANISM Mitochondrion Chaitoregma tattakana
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Paraneoptera; Hemiptera; Sternorrhyncha;
Aphidiformes; Aphidoidea; Hormaphididae; Chaitoregma.
REFERENCE
AUTHORS Fukatsu,T., Shibao,H., Nikoh,N. and Aoki,S.
TITLE Genetically Distinct Populations in an Asian Soldier-Producing
Aphid, Pseudoregma bambucicola (Homoptera: Aphididae), Identified
by DNA Fingerprinting and Molecular Phylogenetic Analysis
Mol. Phylogenet. Evol. 18 (3), 423-433 (2001)
11277634
2 (bases 1 to 1669)
Fukatsu,T. and Nikoh,N.
Direct Submission
JOURNAL Submitted (15-DEC-1999) Takema Fukatsu, National Institute of
Bioscience and Human-Technology, Bioengineering Department; 1-1
Higashi, Tsukuba, Ibaraki 305-8566, Japan
(E-mail: fukatsu@nih.go.jp, Tel:81-298-61-6087, Fax:81-298-61-6080)
FEATURES
source
1..1669
/organism="Chaitoregma tattakana"
/organelle="mitochondrion"
/db_xref="taxon:41909"
<1..426
/product="small subunit rRNA"
427..598
/note="putative location"
/product="trRNA-Val"
599..>1669
/product="large subunit rRNA"
BASE COUNT 687 a 66 c 146 g 770 t
ORIGIN

Query Match 2.7%; Score 55; DB 3; Length 1669;
Best Local Similarity 42.1%; Pred. No. 0.059;
Matches 316; Conservative 0; Mismatches 435; Indels 0; Gaps 0;

Qy 49 aaaaatcaggagaaattataggccattatagagcaactaaataaaatgtgcgttgt 108
Db 1186 AAAAAATTTATACTAATTTAATCATTTTACTATAAAAAAATTTAATTTATAAATTTA 1127

Qy 109 attgaaaaaaacacctattatacaacaacatcgcgaagatacaaatctttttatcacaca 168
Db 1126 ATATAAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1067

Qy 169 actatattgagttctttcttctctgttaactcttatttaataaaacattttggctatta 228
Db 1056 CTTTAAATAAATAAATTTCTATTCTATAAATAATTTAAATTTTAAATAATTTATTA 1007

Qy 229 aataatggcaactaagtttagcaccactgtaattagattttgtctggaaacattttctcga 288
Db 1006 ATTTCAAGCTTATCCCTAAAATAATTTAAATTTAAATAATATAATAAATAAATAA 947

Qy 289 ctaagaagctattggactgtcctcttttgcacaaacaagtagaaaaatggaaacgcctcttaa 348
Db 946 TAACCTTTTAAAAATTTTAAATTTAATTTAATTTAATTTAATTTAATTTAATTTA 887

Qy 349 aaaaacctctcacatcgctgggtgctgaataaaaactgaaacattagcttttttatagct 408
Db 886 TAAATTTTAAACTAAAATTTATTTTAAATATTTTATAAACAATAAATAATATAAATA 827
```



```

Insert size: 138000; pulse-field-gel
Insert size: 148333; sum-of-contigs
Quality coverage: 9.53x in Q20 bases; agarose-fp
Quality coverage: 10.36x in Q20 bases; pulse-field-gel
Quality coverage: 9.63x in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1      3274: contig of 3274 bp in length
*
3275      3374: gap of unknown length
*
3376      8579: contig of 5205 bp in length
*
3377      8580: gap of unknown length
*
3378      8580: gap of unknown length
*
3379      11947: contig of 3267 bp in length
*
3380      12046: gap of unknown length
*
3381      12047: contig of 6714 bp in length
*
3382      18760: contig of 6714 bp in length
*
3383      18761: 18860: gap of unknown length
*
3384      18861: 25184: contig of 6324 bp in length
*
3385      25185: 25284: gap of unknown length
*
3386      25285: 31396: contig of 6112 bp in length
*
3387      31397: 31496: gap of unknown length
*
3388      31497: 37462: contig of 5966 bp in length
*
3389      37463: 37562: gap of unknown length
*
3390      37563: 43999: contig of 6437 bp in length
*
3391      44000: 44099: gap of unknown length
*
3392      44100: 54800: contig of 10701 bp in length
*
3393      54801: 65218: contig of 10318 bp in length
*
3394      65219: 65318: gap of unknown length
*
3395      65319: 76710: contig of 11392 bp in length
*
3396      76711: 76810: gap of unknown length
*
3397      76811: 92005: contig of 15195 bp in length
*
3398      92006: 92105: gap of unknown length
*
3399      92106: 105629: contig of 13524 bp in length
*
3400      105630: 105729: gap of unknown length
*
3401      105730: 122836: contig of 17107 bp in length
*
3402      122837: 122936: gap of unknown length
*
3403      122937: 149733: contig of 26797 bp in length.
*
Location/Qualifiers
1. 149733
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-135M11"
/clone_lib="RP43"
feature 1..3274
/note="assembly_fragment"
feature 3375..8579
/note="assembly_fragment"
feature 8680..11946
/note="assembly_fragment"
feature 12047..18760
/note="assembly_fragment"
feature 18861..25184
/note="assembly_fragment"
feature 25285..31396
/note="assembly_fragment"
feature 31497..37462
/note="assembly_fragment"
feature 37563..43999
/note="assembly_fragment
clone_end:17
vector_side:left"
feature 44100..54800
/note="assembly_fragment"
feature 54901..65218
/note="assembly_fragment"
feature 65319..76710
/note="assembly_fragment"

```

[illegible]

Search completed: December 19, 2001, 22:54:10
Job time: 10491 sec

Query Match	2.5%	Score 51.2;	DB 2;	Length 104992;
Best Local Similarity	48.9%	Pred. No. 0.46;		
Matches 137;	Conservative 0;	Mismatches 143;	Indels 0;	Gaps 0;
Qy 106	tgattgaaaaaaacattattatacaaacacattcgcagaagatacacattctttataac	165		
Db 77042	TATATATAATAAAGTCTCTATTTTTCAAAAAGGTTTCACAATGTAAAAATTTATTTGT	77101		
Qy 166	acaactatagtgaagtctctctctctctgtaacctcttatcaataaaacattttggcta	225		

Result No.	Score	Query %		Length	DB	ID	Description
		Match	Length				
1	2069	100.0	2069	22	AAC5921		MIP synthase promo
2	183.6	8.9	936	22	AAF58252		Oligonucleotide D1
3	183.6	8.9	936	22	AAF58254		Oligonucleotide D1
4	183.6	8.9	936	22	AAF58257		Oligonucleotide D1
5	183.6	8.9	936	22	AAF58259		Oligonucleotide D2
6	183.6	8.9	936	22	AAF58262		Oligonucleotide D2
7	183.6	8.9	936	22	AAF58255		Oligonucleotide D1
c 8	182.8	8.8	936	22	AAF58252		Oligonucleotide D1
c 9	182.8	8.8	936	22	AAF58254		Oligonucleotide D1
c 10	182.8	8.8	936	22	AAF58257		Oligonucleotide D1
c 11	182.8	8.8	936	22	AAF58259		Oligonucleotide D2

[illegible]

[illegible]

Qy - 509 aaaaaagtgttctactgataaaagcagagatgatgtatgaccgtgaccgtgagctaaa 568

Db 15 74

[illegible]

RESULT 8

AAF58252/c
ID AAF58252 standard; DNA: 936 BP.

AC AAF58252:

DT 24-APR-2001 (first entry)

DE Oligonucleotide D1835.

XX Electron-transfer group; ETM; mismatch; genotyping;
KW gene expression: ss.

XX	Synthetic.
OS	Synthetic.

XX WO200107665-A2.

XX PD 01-FEB-2001.

XX
PF 26-JUL-2000; 2000WOLUS20476.

XX 26-JUL-1999: 99US0145695.

PR I/-MAR-2000; 2000US10190259.

[illegible]

(CLIN-) CLINICAL MICRO SENSORS INC.
Umek RM;

WPI; 2001-159728/16.

Nucleic acids containing electron-transfer group, useful as labels in hybridization assays, e.g. for genotyping, allowing repeat analyses on a single surface -

Example 6; Page 127; 159pp; English.

The present invention relates to a composition comprising two nucleic acids each containing an electron-transfer group (ETM) having different redox potentials. The invention is used for electronic detection of nucleic acids, especially of substitutions (mismatches) and single-nucleotide polymorphisms, e.g. for genotyping, monitoring gene expression.

Sequence 936 BP; 4 A; 139 C; 10 G; 7 T; 776 other;

Query Match 8.8%; Score 182.8; DB 22; Length 936;
Best Local Similarity 0.5%; Pred. No. 2.7e-37;

	Matches	4;	Conservative	533;	Mismatches	235;	Indels	0;	Gaps	0;
Qy	29	t	a	a	a	a	a	a	a	88
Db	773	W	W	W	W	W	W	W	W	714
Qy	89	c	t	a	a	a	a	a	a	148
Db	713	W	W	W	W	W	W	W	W	654
Qy	149	a	t	a	c	a	a	a	a	208
Db	653	W	W	W	W	W	W	W	W	594
Qy	209	t	a	a	a	c	a	t	t	268
Db	593	W	W	W	W	W	W	W	W	534
Qy	269	g	t	c	g	a	a	a	a	328
Db	533	W	W	W	W	W	W	W	W	474
Qy	329	a	a	a	t	t	t	a	a	388
Db	473	W	W	W	W	W	W	W	W	414
Qy	389	a	a	c	a	t	t	t	a	448
Db	413	W	W	W	W	W	W	W	W	354
Qy	449	a	t	a	c	c	t	t	a	508
Db	353	W	W	W	W	W	W	W	W	294
Qy	509	a	a	a	a	a	a	a	a	568
Db	293	W	W	W	W	W	W	W	W	234
Qy	569	g	t	c	a	a	a	a	a	628
Db	233	W	W	W	W	W	W	W	W	174
Qy	629	a	t	a	c	a	c	a	c	688
Db	173	W	W	W	W	W	W	W	W	114
Qy	689	g	t	a	a	a	a	a	a	748

PF 26-JUL-2000; 2000WO-US20476.
 XX 26-JUL-1999; 99US-0145695.
 PR 17-MAR-2000; 2000US-0190259.
 XX
 PA (CLIN-) CLINICAL MICRO SENSORS INC.
 XX
 PI Uneik RM;
 XX
 DR WPI; 2001-159728/16.
 XX
 PT Nucleic acids containing electron-transfer group, useful as labels in
 PT hybridization assays, e.g. for genotyping, allowing repeat analyses on
 PT a single surface
 XX
 PS Example 6; Page 127; 159pp; English.
 XX
 CC The present invention relates to a composition comprising two nucleic
 CC acids each containing an electron-transfer group (ETM) having
 CC different redox potentials. The invention is used for electronic
 CC detection of nucleic acids, especially of substitutions (mismatches)
 CC and single-nucleotide polymorphisms, e.g. for genotyping,
 CC monitoring gene expression.
 XX
 SQ Sequence 938 BP; 4 A; 144 C; 9 G; 5 T; 776 other;

Query Match 8.88; Score 182.8; DB 22; Length 938;
 Best Local Similarity 0.58; Pred. No. 2.7e-37;
 Matches 4; Conservative 533; Mismatches 235; Indels 0; Gaps 0;

QY 29 taatatccaatcacaatcctaaatcaggagaaatattatgcatattatagaaacaa 88
 Db 773 WWWWWW
 QY 89 ctaataaaatgctgttattgaaataaaacattattatacaacacatctgccaga 148
 Db 713 WWWWWW
 QY 149 atacaattctttatcacaaactatagtgagctctttcttcttctgtaactctataa 208
 Db 653 WWWWWW
 QY 209 taacaatttttgctattaaatgaatgcaactaagttagcacacactgtaattttt 268
 Db 593 WCVWWWWW
 QY 269 gtctggacaatttctgactaagaagctatttggactgtccctttgccaaacaagtag 328
 Db 533 WWWWWW
 QY 329 aaatggaacgcctccttaaaaaaacattctcacatcgctgggtgctgaataaacgaa 388
 Db 473 WWWWWW
 QY 389 aacattagctttttatgactcgcctcgtctgtagtgattgtttataaaatcattttacca 448
 Db 413 WWWWWW
 QY 449 attaccttttaataaactgtagtatttcatcagtagaactactcacgagagtaaac 508
 Db 353 WWWWWW
 QY 509 aaaaagttgttctactgataaaagcagagatgatgatgacgcgtgacgcgtgagctaaa 568
 Db 293 WWWWWW
 QY 569 gtccaaaaaaaactgctccacaaataacgacaaacaaagtgtgtattgttgccctaa 628
 Db 233 WWWWWW
 QY 629 attacgacactgacaccacagctattattctctctccattatcacaggatgtaact 688

Db 173 WWWWWW
 QY 689 gtaaaaattttgtatgtaaacattttagtaataattgctagcattttagctacgaa 748
 Db 113 WWWWWW
 QY 749 ttattgaaaaaatgtagtattgtttatataataatttaataaaaactgtaaat 800
 Db 53 WWWWWW
 RESULT 14
 AAC35815
 ID AAC35815 standard; DNA; 483 BP.
 XX
 AC AAC35815;
 XX
 DT 17-OCT-2000 (first entry)
 XX
 DE Zea mays DNA fragment SEQ ID NO: 11525.
 XX
 KW Hybridisation assay; genetic mapping; gene expression control;
 KW protein identification; signal transduction pathway; metabolic;
 KW pathway; promoter; termination sequence; corn; ss.
 XX
 OS Zea mays subsp. mays.
 XX
 PN EP1033405-A2.
 XX
 PD 06-SEP-2000.
 XX
 PF 25-FEB-2000; 2000EP-0301439.
 XX
 PR 25-FEB-1999; 99US-0121825.
 PR 05-MAR-1999; 99US-0123180.
 PR 09-MAR-1999; 99US-0123548.
 PR 21-MAR-1999; 99US-0125788.
 PR 25-MAR-1999; 99US-0126264.
 PR 29-MAR-1999; 99US-0126785.
 PR 01-APR-1999; 99US-0127462.
 PR 06-APR-1999; 99US-0128234.
 PR 08-APR-1999; 99US-0128714.
 PR 16-APR-1999; 99US-0129845.
 PR 19-APR-1999; 99US-0130077.
 PR 21-APR-1999; 99US-0130449.
 PR 23-APR-1999; 99US-0130510.
 PR 28-APR-1999; 99US-0130891.
 PR 30-APR-1999; 99US-0131449.
 PR 30-APR-1999; 99US-0132048.
 PR 04-MAY-1999; 99US-0132484.
 PR 05-MAY-1999; 99US-0132485.
 PR 06-MAY-1999; 99US-0132486.
 PR 07-MAY-1999; 99US-0132487.
 PR 11-MAY-1999; 99US-0132863.
 PR 14-MAY-1999; 99US-0134256.
 PR 14-MAY-1999; 99US-0134218.
 PR 14-MAY-1999; 99US-0134219.
 PR 14-MAY-1999; 99US-0134221.
 PR 18-MAY-1999; 99US-0134370.
 PR 19-MAY-1999; 99US-0134941.
 PR 20-MAY-1999; 99US-0135124.
 PR 21-MAY-1999; 99US-0135353.
 PR 24-MAY-1999; 99US-0135629.
 PR 25-MAY-1999; 99US-0136021.
 PR 27-MAY-1999; 99US-0136392.
 PR 28-MAY-1999; 99US-0136782.
 PR 01-JUN-1999; 99US-0137222.
 PR 03-JUN-1999; 99US-0137528.
 PR 04-JUN-1999; 99US-0137502.
 PR 07-JUN-1999; 99US-0137724.
 PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.

PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match
Best Local Similarity 5.9%;
Matches 136; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

Score 122.2; DB 21; Length 483;
Pred. No. 8.4e-22;

QY 1922 ccccgaccacagccccaacaaaggagcgggcgccctctctctccactt 1981

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 19, 2001, 18:34:04 ; Search time 1766.62 Seconds

(without alignments)
12585.058 Million cell updates/sec

Title: us-09-727-628-3

Perfect score: 2069

Sequence: 1 tctagatttttttcaattc.....gggaattaaaggcaaccatgg 2069

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_estc:*
10: gb_estl:*
11: gb_est2:*
12: gb_htc:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
c 1	71	3.4	1101	13	CNS0039G	AL063921 Drosophila
c 2	70.2	3.4	1101	13	CNS0039G	AL063921 Drosophila
c 3	67	3.2	582	10	AI770934	AI770934 606063D12
c 4	64	3.1	1101	13	CNS000E07	AL069440 Drosophila
c 5	58.8	2.8	1101	13	CNS000E07	AL069440 Drosophila
c 6	58.4	2.8	1101	13	CNS000EVL	AL069706 Drosophila
c 7	58	2.8	454	10	AW231748	AW231748 687023G08
c 8	58	2.8	1201	13	CNS0167M	AL106396 Drosophila
c 9	57.4	2.8	1101	13	CNS0021J	AL061936 Drosophila
c 10	56.4	2.7	928	13	CNS000DKY	AL071865 Drosophila
c 11	56	2.7	925	13	CNS00091P	AL053013 Drosophila
c 12	54.8	2.6	500	10	AU086608	AU086608 AU086608

13	54.4	2.6	869	13	CNS01722	AL108680 Drosophila
c 14	53.8	2.6	925	13	CNS00091P	AL053013 Drosophila
c 15	53.4	2.6	987	13	CNS014PQ	AL104456 Drosophila
c 16	53.2	2.6	902	11	BG321216	BG321216 Zm04_05g1
c 17	53	2.6	1248	13	B11336	B11336 F19M10-Sp6
c 18	52.8	2.6	1101	13	CNS00BO1	AL057419 Drosophila
c 19	52.2	2.5	1001	13	CNS01400	AL103554 Drosophila
c 20	52.2	2.5	1101	13	CNS00YWL	AL069927 Drosophila
c 21	52.2	2.5	1200	13	CNS016CO	AL106578 Drosophila
c 22	52.2	2.5	1225	13	CNS0161D	AL106171 Drosophila
c 23	51.6	2.5	975	13	CNS0102Y	AL098452 Drosophila
c 24	51.4	2.5	867	13	CNS075BG	AL429890 clone BA0
c 25	51.2	2.5	912	13	CNS006N3	AL065775 Drosophila
c 26	51.2	2.5	994	13	CNS015XG	AL106030 Drosophila
c 27	51.2	2.5	1101	13	CNS000D1	AL065414 Drosophila
c 28	51.2	2.5	1101	13	CNS00LVZ	AL078819 Drosophila
c 29	51.2	2.5	1101	13	CNS002BM	AL097468 Drosophila
c 30	51	2.5	1099	10	AL536986	AL536986 AL536986
c 31	51	2.5	1101	13	CNS00EVL	AL069706 Drosophila
c 32	50.8	2.5	1051	10	AL535414	AL535414 AL535414
c 33	50.8	2.5	1101	13	CNS002ZU	AL097152 Drosophila
c 34	50.6	2.4	500	10	AU087038	AU087038 AU087038
c 35	50.6	2.4	976	13	CNS04ESM	AL286627 Tetraodon
c 36	50.4	2.4	713	13	CNS06C1J	AL392561 T7 end of
c 37	50.4	2.4	928	13	CNS00DKY	AL071865 Drosophila
c 38	50.4	2.4	1101	13	CNS00YWL	AL069927 Drosophila
c 39	50.4	2.4	1384	11	BF033991	BF033991 601456301
c 40	50.2	2.4	1101	13	CNS000D7	AL075293 Drosophila
c 41	50	2.4	942	13	CNS018GS	AL109318 Drosophila
c 42	50	2.4	1101	13	CNS017SY	AL108460 Drosophila
c 43	50	2.4	1225	13	CNS0161D	AL106171 Drosophila
c 44	49.8	2.4	631	10	AL566993	AL566993 AL566993
c 45	49.8	2.4	749	13	AQ794523	AQ794523 nbxb0053M

ALIGNMENTS

RESULT 1
CNS0039G/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CNS0039G 1101 bp DNA GSS
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
AL063921
AL063921.1 GI:4941778
GSS.
fruit fly.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see <http://www.fruitfly.org> The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammose in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2: cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.


```

Db      235 CGAAAGAGGGGAGGAA 251
||||| |||| | ||| |
RESULT   4
CNS00E07/c
LOCUS    CNS00E07          1101 bp      DNA           GSS            04-JUN-1999
DEFINITION Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR29P01 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL069440.1 GI:494583
VERSION    AL069440.1
KEYWORDS   fruit fly.
SOURCE     Drosophila melanogaster
ORGANISM   Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
            Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE  1 (bases 1 to 1101)
AUTHORS    Genoscope.
TITLE       Direct Submission
JOURNAL     Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage ;
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
COMMENT    Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mamoser in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain y2; cn bw sp, the same strain used for the BDGP's
PI and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES             Location/Qualifiers
     source           1..1101
                     /organism="Drosophila melanogaster"
                     /db_xref="taxon:7227"
                     /clone_lib="RPCI-98"
                     /clones="BACR29P01"
                     /notes="end : TET3"

BASE COUNT  366 a   66 c   104 g   351 t   214 others

ORIGIN

Query Match              3.1%; Score 64; DB 13; Length 1101;
Best Local Similarity  37.6%; Pred. No. 0.0017;
Matches 172; Conservative 62; Mismatches 219; Indels 4; Gaps 1

Qy  2 ctgatttttttccaattcaccccgagtaaatcacaatcctcaaaatcaggaga 61
    |:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db  973 CAWWAYATTTTWTATACATAATTTTTTTTATACAAATTTWAAAATAAACCAWA 914

Qy  62 aattatggccattattagaagcaactaaaataaagtgcgttgattgaaaaaaaa 121
    |:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db  913 ATTTAWAANAACATTWTTTTAAWTAATTTTATTCACW-----TWTATAAAAAAAT 858

Qy  122 ccattataaacaacatctgccagaatacaactcttttatcacacaactatgtgag 181
    |:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db  857 TAAAWTAANAARAAARWATTAATTTATYATWATATWTAAAWWTATATATTTWWAAT 798

Qy  182 ttcttttctctgttaacctctattataaaacaatttttggctattaataatggcaact 241
    |:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db  797 WTTATANNATTTTTTTTTTAWAATTTTWTATWATWATTAATTTTAAWTWTTTAAATAAAAAA 738

Qy  242 aagtagcaccactgtaattgatgttttgtcggacaactttctcgtactaagaagctatt 301
    |:|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db  737 ATTTATTTTTTTATTTWATTAATAAATTTTTTTTAAATTTTWTTTAAATTTTAAATTTT 678

```

[illegible]

project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelOBAC11.

```
FEATURES
  source
    1. .1201
    /organism="Drosophila melanogaster"
    /plasmid="pBelOBAC11"
    /db_xref="taxon:7227"
    /clone_lib="DrosBAC"
    /clone="BACN15M24"
    /note="end : T7"
BASE COUNT      323 a      87 c      79 g      551 t      161 others
ORIGIN
Query Match      2.8%; Score 58; DB 13; Length 1201;
Best Local Similarity 37.0%; Pred. No. 0.033;
Matches 211; Conservative 60; Mismatches 293; Indels 7; Gaps 1;
QY 39 atcaaatctaaatacagagaaattatatggccattattagaagcaactaaataaaa 98
Db 1184 ATATAATATAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 1125
QY 99 tggcggtgtgattgaaataaaacattttatacaaacatctgcgaagaatacaattct 158
Db 1124 ATAAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAWAAW 1065
QY 159 ttatacaacaacttatgtgagttctttctctgtgaactcttattataaacaattt 218
Db 1064 ANAATATTTTWTNTATAWAATTTTATTAATAAATAAATAAATAAATAAATAA 1005
QY 219 ttggctattaaataatggcaactaagttagcaccatgttaatttagattttgtctggaaca 278
Db 1004 TTTAAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 945
QY 279 attctctgactgaagaagctattgactgctcttgcgaacaagtagaagaatggaac 338
Db 944 AWAATATWAAWTTTATTTATWATATAAATAAATAAATAAATAAATAAATAAATAA 805
QY 339 cgctccttaaaacaccatctcacatcgctgggtgctgataaaactgaaacattagct 398
Db 884 A-----ATWTAATAATATAAATAAATAAATAAATAAATAAATAAATAAATAA 832
QY 399 ttctatgctcgtcgtcgtcgtatgtgttataaaatcattttaccattacacattt 458
Db 831 ATTATAAATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 772
QY 459 taaactgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 518
Db 771 WAAAAATWTAATAATATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 712
QY 519 gtctactgataaagcagagatgatgtatgacggtgacggtgacggtgacggtgacggt 578
Db 711 AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 652
QY 579 aaaaactgctccacaataacgacaaacaaa 609
Db 651 AMACMAMMTAAAGCNTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 621
```

```
RESULT 9
CNS0021J CNS0021J 1101 bp DNA GSS 03-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence TET3 end of BAC #
DEFINITION BACR05N11 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL061936
VERSION AL061936
KEYWORDS fruit fly.
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
```

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

FEATURES
source

BASE COUNT 631 a 7 c 28 g 289 t 146 others
ORIGIN

Query Match 2.8%; Score 57.4; DB 13; Length 1101;
Best Local Similarity 44.1%; Pred. No. 0.044;
Matches 130; Conservative 20; Mismatches 145; Indels 0; Gaps 0;

```
QY 30 aaatatccaatcacatctcaaaatcaggagaaattatatggccattattagaagcaac 89
Db 395 AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 454
QY 90 taaataaaatgctgctgtattgaaataaaacattttatacaaacatctgcgaagaa 149
Db 455 AAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 514
QY 150 tacaattctttatcacacacttatgtgagttctttctctgttaactcttattat 209
Db 515 TATAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 574
QY 210 aaacatttttggctattataataatggcaactaagtagcaccactgttaatttagatttg 269
Db 575 AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 634
QY 270 tctggaacaattctctgactgaagaagctatttggagctgctcttttgcgaacaaa 324
Db 635 TWTTTTWTTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 689
```

```
RESULT 10
CNS00DKY/c CNS00DKY 928 bp DNA GSS 04-JUN-1999
LOCUS Drosophila melanogaster genome survey sequence T7 end of BAC #
DEFINITION BACR27A24 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION AL071865
VERSION AL071865
KEYWORDS fruit fly.
SOURCE Drosophila melanogaster
ORGANISM Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 928)
```

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
Genoscope.
Direct Submission
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see <http://www.fruitfly.org> The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoler in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's p1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

THIS PAGE BLANK (USPTO)